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RAW SEQUENCE LISTING

DATE: 06/17/2003

PATENT APPLICATION: US/09/508,849A

TIME: 07:40:19

Input Set : A:\2003-06-09 1110-0266P.ST25.txt

Output Set: N:\CRF4\06172003\I508849A.raw

3 <110> APPLICANT: NAGATA, Shigekazu
4 TANAKA, Masato
6 <120> TITLE OF INVENTION: Novel Fas Ligand Derivative
8 <130> FILE REFERENCE: 1110-0266P
10 <140> CURRENT APPLICATION NUMBER: 09/508,849A
11 <141> CURRENT FILING DATE: 2001-03-17
13 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04187
14 <151> PRIOR FILING DATE: 1998-09-17
16 <150> PRIOR APPLICATION NUMBER: JP 9-252541
17 <151> PRIOR FILING DATE: 1997-09-17
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 258
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: amino acids at
30 111-133 from N terminal are deleted from natural
31 human Fas ligand
33 <400> SEQUENCE: 1
34 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
35 1 5 10 15
37 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
38 20 25 30
40 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
41 35 40 45
43 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
44 50 55 60
46 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
47 65 70 75 80
49 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
50 85 90 95
52 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Pro Ser
53 100 105 110
55 Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly
56 115 120 125
58 Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly
59 130 135 140
61 Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile
62 145 150 155 160
64 Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly
65 165 170 175

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67 Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn
68          180          185          190
70 Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser
71          195          200          205
73 Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala
74          210          215          220
76 Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu
77 225          230          235          240
79 Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr
80          245          250          255
82 Lys Leu
86 <210> SEQ ID NO: 2
87 <211> LENGTH: 277
88 <212> TYPE: PRT
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Description of Artificial Sequence:amino acids at
93     128-131 from N terminal are deleted from natural
94     human Fas ligang
96 <400> SEQUENCE: 2
97 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
98   1          5          10          15
100 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
101          20          25          30
103 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
104          35          40          45
106 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
107          50          55          60
109 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
110 65          70          75          80
112 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
113          85          90          95
115 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
116          100          105          110
118 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Gly
119          115          120          125
121 His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His
122          130          135          140
124 Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp
125 145          150          155          160
127 Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly
128          165          170          175
130 Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr
131          180          185          190
133 Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr
134          195          200          205
136 Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys
137          210          215          220
139 Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr

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140 225          230          235          240
142 Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn
143          245          250          255
145 Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe
146          260          265          270
148 Gly Leu Tyr Lys Leu
149          275
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 281
154 <212> TYPE: PRT
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence:point mutation
159 of a substitution of Lys 129 for Ala from N
160 terminal is present in natural human Fas ligand
161
163 <400> SEQUENCE: 3
164 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
165 1 5 10 15
167 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
168 20 25 30
170 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
171 35 40 45
173 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
174 50 55 60
176 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
177 65 70 75 80
179 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
180 85 90 95
182 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
183 100 105 110
185 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
186 115 120 125
188 Ala Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
189 130 135 140
191 Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
192 145 150 155 160
194 Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
195 165 170 175
197 Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
198 180 185 190
200 Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
201 195 200 205
203 His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
204 210 215 220
206 Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
207 225 230 235 240
209 Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
210 245 250 255

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212 Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
213           260           265           270
215 Gln Thr Phe Phe Gly Leu Tyr Lys Leu
216           275           280
219 <210> SEQ ID NO: 4
220 <211> LENGTH: 774
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
226     amino acids SEQ ID No.1
228 <400> SEQUENCE: 4
229 atgcagcagc ccttcaatta cccatatccc cagatctact ggggtggacag cagtgccagc 60
230 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
231 ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
232 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaaacca cagcacaggc 240
233 ctgtgtctcc ttgtgatgtt ttcatggtt ctggttgcc tggtaggatt gggcctggg 300
234 atgtttcagc tcttccacct acagaaggag ccagtgccac cccctgaaaa aaaggagctg 360
235 aggaaagtgg ccattttaac aggcaagtcc aactcaaggt ccatgcctct ggaatgggaa 420
236 gacacctatg gaattgtcct gctttctgga gtgaagtata agaaggggtg ccttgtgatc 480
237 aatgaaactg ggctgtactt tgtatattcc aaagtatact tccgggggtc atcttgaac 540
238 aacctgcccc tgagccacaa ggtctacatg aggaactcta agtatcccca ggatctggg 600
239 atgatggagg ggaagatgat gagctactgc actactgggc agatgtgggc ccgcagcagc 660
240 tacctggggg cagtgttcaa tcttaccagt gctgatcatt tatatgtcaa cgtatctgag 720
241 ctctctctgg tcaattttga ggaatctcag acgtttttcg gcttatataa gctc 774
244 <210> SEQ ID NO: 5
245 <211> LENGTH: 831
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
251     amino acids SEQ ID No.2
253 <400> SEQUENCE: 5
254 atgcagcagc ccttcaatta cccatatccc cagatctact ggggtggacag cagtgccagc 60
255 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
256 ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
257 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaaacca cagcacaggc 240
258 ctgtgtctcc ttgtgatgtt ttcatggtt ctggttgcc tggtaggatt gggcctggg 300
259 atgtttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
260 atgcacacag catcatcttt gggccacccc agtccacccc ctgaaaaaaaa ggagctgagg 420
261 aaagtggccc atttaacagg caagtccaac tcaaggtcca tgcctctgga atgggaagac 480
262 acctatggaa ttgtcctgct ttctggagtg aagtataaga aggggtggcct tgtgatcaat 540
263 gaaactgggc tgtactttgt atattccaaa gtatacttcc ggggtcaatc ttgcaacaac 600
264 ctgcccctga gccacaaggt ctacatgagg aactctaagt atccccagga tctggtgatg 660
265 atggagggga agatgatgag ctactgcact actgggcaga tgtgggcccg cagcagctac 720
266 ctgggggcag tgttcaatct taccagtgtc gatcatttat atgtcaacgt atctgagctc 780
267 tctctgggtc attttgagga atctcagacg tttttcggct tatataagct c 831
270 <210> SEQ ID NO: 6
271 <211> LENGTH: 843

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272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
277     amino acids SEQ ID No.3
279 <400> SEQUENCE: 6
280 atgcagcagc ccttcaatta cccatatccc cagatctact ggggtggacag cagtgccagc 60
281 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
282 ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
283 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaacca cagcacaggc 240
284 ctgtgtctcc ttgtgatgtt ttcatgtgtt ctggttgcct tggtaggatt gggcctgggg 300
285 atgtttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
286 atgcacacag catcatcttt ggaggcacia ataggccacc ccagtccacc ccctgaaaaa 420
287 aaggagctga ggaaagtggc ccatttaaca ggcaagtcca actcaaggtc catgcctctg 480
288 gaatgggaag acacctatgg aattgtcctg ctttctggag tgaagtataa gaagggtggc 540
289 cttgtgatca atgaaactgg gctgtacttt gtatatccaa aagtatactt ccgggggtcaa 600
290 tcttgcaaca acctgccccct gagccacaag gtctacatga ggaactctaa gtatccccag 660
291 gatctggtga tgatggaggg gaagatgatg agctactgca ctactgggca gatgtgggcc 720
292 cgcagcagct acctgggggc agtgttcaat cttaccagtg ctgatcattt atatgtcaac 780
293 gtatctgagc tctctctggt caattttgag gaatctcaga cgtttttcgg cttatataag 840
294 ctc
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 20
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence:a sense primer
303     BOS6
305 <400> SEQUENCE: 7
306 cctcagacag tggttcaaag
309 <210> SEQ ID NO: 8
310 <211> LENGTH: 39
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence:an antisense
316     deletion primer DA4
318 <400> SEQUENCE: 8
319 ttttcagggg gtggactggg ctccttctgt aggtggaag
322 <210> SEQ ID NO: 9
323 <211> LENGTH: 28
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence:HFLP3
330 <400> SEQUENCE: 9
331 gctctagaac attctcggtg cctgtaac
334 <210> SEQ ID NO: 10
335 <211> LENGTH: 30

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VERIFICATION SUMMARY

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